

## Research Article

## DGGE and real-time PCR analysis of lactic acid bacteria in bacterial communities of the phyllosphere of lettuce

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Food associated indigenous microbial communities exert antagonistic effects on pathogens and may routinely deliver health relevant microorganisms to the GI tract. By using molecular, culture independent methods including PCR-DGGE of 16S rDNA-coding regions and real-time PCR (RT-PCR) as well as BIOLOG metabolic fingerprinting, microbial communities on lettuce were analyzed in samples from fields, from supermarkets and soil. Amplified 16S rRNA gene sequences (57.7%) could be assigned to species previously reported as typical for the phyllosphere including *Pantoea agglomerans*, *Pseudomonas fluorescens*, *Moraxella* spp., and *Mycobacterium* spp. 71.8% of the sequences obtained represented so far undescribed taxa. Principal component analysis of BIOLOG metabolic profiles indicated a seasonal variation in the lettuce phyllosphere microbial community structure. Various lactic acid bacteria were detected including several *Lactobacillus* and *Leuconostoc* species in particular on lettuce from organic farming. By RT-PCR lactobacilli were found with a range of abundances from  $1 \times 10^4$  to  $1 \times 10^5$  copies/g lettuce. Considering the importance of salad in many diets lettuce may contribute to a constant supply with LAB.

**Keywords:** DGGE / Lactic acid bacteria / Organic agriculture / Phyllosphere / RT-PCR

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